

FEATURE ARTICLES

GENETIC CHARACTERIZATION OF COMMON EIDERS BREEDING IN THE YUKON-KUSKOKWIM DELTA, ALASKA

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Abstract. We assessed population genetic subdivision among four colonies of Common Eiders (*Somateria mollissima v-nigrum*) breeding in the Yukon-Kuskokwim Delta (YKD), Alaska, using microsatellite genotypes and DNA sequences with differing modes of inheritance. Significant, albeit low, levels of genetic differentiation were observed between mainland populations and Kigigak Island for nuclear intron *lamin A* and mitochondrial DNA (mtDNA) control region. Intercolony variation in haplotypic frequencies also was observed at mtDNA. Positive growth signatures assayed from microsatellites, nuclear introns, and mtDNA indicate recent colonization of the YKD, and may explain the low levels of structuring observed. Gene flow estimates based on microsatellites, nuclear introns, and mtDNA suggest asymmetrical gene flow between mainland colonies and Kigigak Island, with more individuals on average dispersing from mainland populations to Kigigak Island than vice versa. The directionality of gene flow observed may be explained by the colonization of the YKD from northern glacial refugia or by YKD metapopulation dynamics.

Key words: Common Eider, gene flow, population genetic structure, *Somateria mollissima*.